

SEQUENCE LISTING

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<120> Controlling Starch Synthesis

<130> U-013220-5

<140> US 09/744,085
<141> 2001-03-26

<150> PCT/IL99/00396
<151> 1999-07-19

<150> IL 125425
<151> 1998-07-20

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<170> PatentIn Ver. 2.1

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1 5 10 15

aat gga gag aag gag att ttt ggg gag aag atg aga ggg agt ttg aac 96

Asn	Gly	Glu	Lys	Glu	Ile	Phe	Gly	Glu	Lys	Met	Arg	Gly	Ser	Leu	Asn	
20								25							30	
aac	aat	ctc	agg	att	aat	cag	ttg	tcg	aaa	agt	ttg	aaa	ctt	gag	aag	144
Asn	Asn	Leu	Arg	Ile	Asn	Gln	Leu	Ser	Lys	Ser	Leu	Lys	Leu	Glu	Lys	
35								40							45	
aag	gag	aag	aag	att	aaa	cct	ggg	gtt	gct	tac	tct	gtg	atc	act	act	192
Lys	Glu	Lys	Lys	Ile	Lys	Pro	Gly	Val	Ala	Tyr	Ser	Val	Ile	Thr	Thr	
50								55							60	
gaa	aat	gac	aca	gag	act	gtg	ttc	gta	gat	atg	cca	cgt	ctt	gag	aga	240
Glu	Asn	Asp	Thr	Glu	Thr	Val	Phe	Val	Asp	Met	Pro	Arg	Leu	Glu	Arg	
65							70				75				80	
cgc	cg	gca	aat	ccc	aag	gat	gtg	gct	gca	gtc	ata	tta	gga	gga	ggc	288
Arg	Arg	Ala	Asn	Pro	Lys	Asp	Val	Ala	Ala	Val	Ile	Leu	Gly	Gly	Gly	
85							90								95	
gaa	ggg	acc	aag	tta	ttc	cca	ctt	aca	agt	aga	act	gca	acc	cct	gct	336
Glu	Gly	Thr	Lys	Leu	Phe	Pro	Leu	Thr	Ser	Arg	Thr	Ala	Thr	Pro	Ala	
100							105								110	
gtt	ccg	gtt	gga	gga	tgc	tac	agg	ctc	ata	gac	atc	ccg	atg	agc	aac	384
Val	Pro	Val	Gly	Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	
115							120								125	
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Cys	Ile	Asn	Ser	Ala	Ile	Asn	Lys	Ile	Phe	Val	Leu	Thr	Gln	Tyr	Asn	
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tct	gct	gcc	ctg	aat	cgt	cac	att	gct	cga	acg	tat	ttt	ggc	aat	ggt	480
Ser	Ala	Ala	Leu	Asn	Arg	His	Ile	Ala	Arg	Thr	Tyr	Phe	Gly	Asn	Gly	
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Val	Ser	Phe	Gly	Asp	Gly	Phe	Val	Glu	Val	Leu	Ala	Ala	Thr	Gln	Thr	
165							170								175	
cct	ggg	gaa	gca	gga	aaa	aaa	tgg	ttt	caa	gga	aca	gca	gat	gct	gtc	576
Pro	Gly	Glu	Ala	Gly	Lys	Lys	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ala	Val	
180							185								190	
aga	aaa	ttt	ata	tgg	gtt	ttt	gag	gac	gct	aag	aac	aag	aat	att	gaa	624
Arg	Lys	Phe	Ile	Trp	Val	Phe	Glu	Asp	Ala	Lys	Asn	Lys	Asn	Ile	Glu	
195							200								205	
aat	atc	ctt	gta	tta	tct	ggg	gat	cat	ctt	tat	agg	atg	gat	tat	atg	672
Asn	Ile	Leu	Val	Leu	Ser	Gly	Asp	His	Leu	Tyr	Arg	Met	Asp	Tyr	Met	
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DNA SEQUENCING

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Ile Asp Ser Arg Gly Arg Val Val Gln Phe Ala Glu Lys Pro Lys Gly			
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ttt gag ctt aaa gca atg caa gta gat act act ctt gtt gga tta tct		864	
Phe Glu Leu Lys Ala Met Gln Val Asp Thr Thr Leu Val Gly Leu Ser			
275	280	285	
cca caa gat gcg aag aaa tcc cct tat att gct tca atg gga gtt tat		912	
Pro Gln Asp Ala Lys Lys Ser Pro Tyr Ile Ala Ser Met Gly Val Tyr			
290	295	300	
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Val Phe Lys Thr Asp Val Leu Leu Lys Leu Leu Lys Trp Ser Tyr Pro			
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Thr Ser Asn Asp Phe Gly Ser Glu Ile Ile Pro Ala Ala Ile Asp Asp			
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tac aat gtc caa gca tac att ttc aaa gac tat tgg gag gac att gga		1056	
Tyr Asn Val Gln Ala Tyr Ile Phe Lys Asp Tyr Trp Glu Asp Ile Gly			
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aca att aaa tct ttc tat aat gct agc ttg gcg ctc aca caa gag ttt		1104	
Thr Ile Lys Ser Phe Tyr Asn Ala Ser Leu Ala Leu Thr Gln Glu Phe			
355	360	365	
cca gag ttc caa ttt tat gat cca aaa aca cct ttt tac aca tct cct		1152	
Pro Glu Phe Gln Phe Tyr Asp Pro Lys Thr Pro Phe Tyr Thr Ser Pro			
370	375	380	
agg ttc ctt cca cca acc aag ata gac aat tgc aag att aag gat gcc		1200	
Arg Phe Leu Pro Pro Thr Lys Ile Asp Asn Cys Lys Ile Lys Asp Ala			
385	390	395	400
ata att tct cat gga tgt ttc ttg cga gat tgc tct gtg gaa cac tcc		1248	
Ile Ile Ser His Gly Cys Phe Leu Arg Asp Cys Ser Val Glu His Ser			
405	410	415	
ata gtg ggt gaa aga tca cgc tta gac tgt ggt gtt gaa ctg aag gat		1296	
Ile Val Gly Glu Arg Ser Arg Leu Asp Cys Gly Val Glu Leu Lys Asp			
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Thr Phe Met Met Gly Ala Asp Tyr Tyr Gln Thr Glu Ser Glu Ile Ala			
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Ser Leu Leu Ala Glu Gly Lys Val Pro Ile Gly Ile Gly Glu Asn Thr			
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465	470	475	480
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Val Ser Ile Ile Asn Lys Asp Gly Val Gln Glu Ala Asp Arg Pro Glu			
485	490	495	
gaa gga ttc tac ata cga tca ggg ata acc att ata tca gag aaa gcc			1536
Glu Gly Phe Tyr Ile Arg Ser Gly Ile Thr Ile Ile Ser Glu Lys Ala			
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Val Pro Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn			
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Arg Lys Phe Ile Trp Val Phe Glu Asp Ala Lys Asn Lys Asn Ile Glu
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210 215 220

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225 230 235 240

Cys Ala Pro Ala Glu Asp Ser Arg Ala Ser Asp Phe Gly Leu Val Lys
245 250 255

Ile Asp Ser Arg Gly Arg Val Val Gln Phe Ala Glu Lys Pro Lys Gly
260 265 270

Phe Glu Leu Lys Ala Met Gln Val Asp Thr Thr Leu Val Gly Leu Ser
275 280 285

Pro Gln Asp Ala Lys Lys Ser Pro Tyr Ile Ala Ser Met Gly Val Tyr
290 295 300

Val Phe Lys Thr Asp Val Leu Leu Lys Leu Leu Lys Trp Ser Tyr Pro
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Thr Ser Asn Asp Phe Gly Ser Glu Ile Ile Pro Ala Ala Ile Asp Asp
325 330 335

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340 345 350

Thr Ile Lys Ser Phe Tyr Asn Ala Ser Leu Ala Leu Thr Gln Glu Phe
355 360 365

Pro Glu Phe Gln Phe Tyr Asp Pro Lys Thr Pro Phe Tyr Thr Ser Pro
370 375 380

Arg Phe Leu Pro Pro Thr Lys Ile Asp Asn Cys Lys Ile Lys Asp Ala
385 390 395 400

Ile Ile Ser His Gly Cys Phe Leu Arg Asp Cys Ser Val Glu His Ser
405 410 415

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Thr Phe Met Met Gly Ala Asp Tyr Tyr Gln Thr Glu Ser Glu Ile Ala
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Lys Ile Arg Lys Cys Ile Ile Asp Lys Asn Ala Lys Ile Gly Lys Asn

465

470

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515 520